

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: McCarthy, Sean
- (ii) TITLE OF INVENTION: NOVEL CRSP-1 COMPOSITIONS AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 - (B) STREET: One Post Office Square
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-2170
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/842,898
 - (B) FILING DATE: 17-APR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Arnold, Beth E.
 - (B) REGISTRATION NUMBER: 35,430
 - (C) REFERENCE/DOCKET NUMBER: MAA-004.02
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 617-832-1000
 - (B) TELEFAX: 617-832-7000

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 38..1087
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG GGC GGCGGCT GCGGGCGCAG AGCGGAG ATG CAG CGG CTT GGG GCC 55
Met Gln Arg Leu Gly Ala
1 5

ACC CTG CTG TGC CTG CTG CTG GCG GCG GCG GTC CCC ACG GCC CCC GCG 103
Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala
10 15 20

CCC GCT CCG ACG GCG ACC TCG GCT CCA GTC AAG CCC GGC CCG GCT CTC 151
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
25 30 35

AGC TAC CCG CAG GAG GAG GCC ACC CTC AAT GAG ATG TTC CGC GAG GTT 199
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
40 45 50

GAG GAA CTG ATG GAG GAC ACG CAG CAC AAA TTG CGC AGC GCG GTG GAA 247
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
55 60 65 70

GAG ATG GAG GCA GAA GAA GCT GCT GCT AAA GCA TCA TCA GAA GTG AAC 295
Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn
75 80 85

CTG GCA AAC TTA CCT CCC AGC TAT CAC AAT GAG ACC AAC ACA GAC ACG 343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr
90 95 100

AAC GTT GGA AAT AAT ACC ATC CAT GTG CAC CGA GAA ATT CAC AAG ATA 391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile
105 110 115

ACC AAC AAC CAG ACT GGA CAA ATG GTC TTT TCA GAG ACA GTT ATC ACA 439
Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr
120 125 130

TCT GTG GGA GAC GAA GAA GGC AGA AGG AGC CAC GAG TGC ATC ATC GAC 487
Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp
135 140 145 150

GAG GAC TGT GGG CCC AGC ATG TAC TGC CAG TTT GCC AGC TTC CAG TAC 535
Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr
155 160 165

ACC TGC CAG CCA TGC CGG GGC CAG AGG ATG CTC TGC ACC CGG GAC AGT 583
Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser
170 175 180

GAG TGC TGT GGA GAC CAG CTG TGT GTC TGG GGT CAC TGC ACC AAA ATG 631
Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met
185 190 195

GCC ACC AGG GGC AGC AAT GGG ACC ATC TGT GAC AAC CAG AGG GAC TGC 679
Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys
200 205 210

CAG CCG GGG CTG TGC TGT GCC TTC CAG AGA GGC CTG CTG TTC CCT GTG 727
Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val
215 220 225 230

TGC ACA CCC CTG CCC GTG GAG GGC GAG CTT TGC CAT GAC CCC GCC AGC 775
 Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser
 235 240 245

CGG CTT CTG GAC CTC ATC ACC TGG GAG CTA GAG CCT GAT GGA GCC TTG 823
 Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu
 250 255 260

GAC CGA TGC CCT TGT GCC AGT GGC CTC CTC TGC CAG CCC CAC AGC CAC 871
 Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His
 265 270 275

AGC CTG GTG TAT GTG TGC AAG CCG ACC TTC GTG GGG AGC CGT GAC CAA 919
 Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln
 280 285 290

GAT GGG GAG ATC CTG CTG CCC AGA GAG GTC CCC GAT GAG TAT GAA GTT 967
 Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val
 295 300 305 310

GGC AGC TTC ATG GAG GAG GTG CGC CAG GAG CTG GAG GAC CTG GAG AGG 1015
 Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg
 315 320 325

AGC CTG ACT GAA GAG ATG GCG CTG AGG GAG CCT GCG GCT GCC GCC GCT 1063
 Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala Ala
 330 335 340

GCA CTG CTG GGA AGG GAA GAG ATT TAGATCTGGA CCAGGCTGTG GGTAGATGTG 1117
 Ala Leu Leu Gly Arg Glu Glu Ile
 345 350

CAATAGAAAT AGCTAATTTA TTTCCCCANG TGTGTGCTTT AAGCGTGGGC TG 1169

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
 1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
 20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
 35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
 50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95

Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
325 330 335

Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile
340 345 350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCAGCGGC TTGGGGCCAC CCTGCTGTGC CTGCTGCTGG CGGCGGCGGT CCCCACGGCC 60
 CCCGCGCCCG CTCCGACGGC GACCTCGGCT CCAGTCAAGC CCGGCCCGGC TCTCAGCTAC 120
 CCGCAGGAGG AGGCCACCCT CAATGAGATG TTCCGCGAGG TTGAGGAACT GATGGAGGAC 180
 ACGCAGCACA AATTGCGCAG CGCGGTGGAA GAGATGGAGG CAGAAGAAGC TGCTGCTAAA 240
 GCATCATCAG AAGTGAACCT GGCAAACCTTA CCTCCCAGCT ATCACAATGA GACCAACACA 300
 GACACGAACG TTGGAAATAA TACCATCCAT GTGCACCGAG AAATTCACAA GATAACCAAC 360
 AACCAGACTG GACAAATGGT CTTTTCAGAG ACAGTTATCA CATCTGTGGG AGACGAAGAA 420
 GGCAGAAGGA GCCACGAGTG CATCATCGAC GAGGACTGTG GGCCCAGCAT GTACTGCCAG 480
 TTTGCCAGCT TCCAGTACAC CTGCCAGCCA TGCCGGGGCC AGAGGATGCT CTGCACCCGG 540
 GACAGTGAGT GCTGTGGAGA CCAGCTGTGT GTCTGGGGTC ACTGCACCAA AATGGCCACC 600
 AGGGGCAGCA ATGGGACCAT CTGTGACAAC CAGAGGGACT GCCAGCCGGG GCTGTGCTGT 660
 GCCTTCCAGA GAGGCCTGCT GTTCCCTGTG TGCACACCCC TGCCCGTGGA GGGCGAGCTT 720
 TGCCATGACC CCGCCAGCCG GCTTCTGGAC CTCATCACCT GGGAGCTAGA GCCTGATGGA 780
 GCCTTGGACC GATGCCCTTG TGCCAGTGGC CTCCTCTGCC AGCCCCACAG CCACAGCCTG 840
 GTGTATGTGT GCAAGCCGAC CTTCGTGGGG AGCCGTGACC AAGATGGGGA GATCCTGCTG 900
 CCCAGAGAGG TCCCCGATGA GTATGAAGTT GGCAGCTTCA TGGAGGAGGT GCGCCAGGAG 960
 CTGGAGGACC TGGAGAGGAG CCTGACTGAA GAGATGGCGC TGAGGGAGCC TGCGGCTGCC 1020
 GCCGCTGCAC TGCTGGGAAG GGAAGAGATT 1050

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Arg Gly Glu Gly Pro Ala Pro Arg Arg Arg Trp Leu Leu Leu
 1 5 10 15
 Leu Ala Val Leu Ala Ala Leu Cys Cys Ala Ala Ala Gly Ser Gly Gly
 20 25 30

Arg Arg Arg Ala Ala Ser Leu Gly Glu Met Leu Arg Glu Val Glu Ala
 35 40 45
 Leu Met Glu Asp Thr Gln His Lys Leu Arg Asn Ala Val Gln Glu Met
 50 55 60
 Glu Ala Glu Glu Glu Gly Ala Lys Lys Leu Ser Glu Val Asn Phe Glu
 65 70 75 80
 Asn Leu Pro Pro Thr Tyr His Asn Glu Ser Asn Thr Glu Thr Arg Ile
 85 90 95
 Gly Asn Lys Thr Val Gln Thr His Gln Glu Ile Asp Lys Val Thr Asp
 100 105 110
 Asn Arg Thr Gly Ser Thr Ile Phe Ser Glu Thr Ile Ile Thr Ser Ile
 115 120 125
 Lys Gly Gly Glu Asn Lys Arg Asn His Glu Cys Ile Ile Asp Glu Asp
 130 135 140
 Cys Glu Thr Gly Lys Tyr Cys Gln Phe Ser Thr Phe Glu Tyr Lys Cys
 145 150 155 160
 Gln Pro Cys Lys Thr Gln His Thr His Cys Ser Arg Asp Val Glu Cys
 165 170 175
 Cys Gly Asp Gln Leu Cys Val Trp Gly Glu Cys Arg Lys Ala Thr Ser
 180 185 190
 Arg Gly Glu Asn Gly Thr Ile Cys Glu Asn Gln His Asp Cys Asn Pro
 195 200 205
 Gly Thr Cys Cys Ala Phe Gln Lys Glu Leu Leu Phe Pro Val Cys Thr
 210 215 220
 Pro Leu Pro Glu Glu Gly Glu Pro Cys His Asp Pro Ser Asn Arg Leu
 225 230 235 240
 Leu Asn Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Val Leu Glu Arg
 245 250 255
 Cys Pro Cys Ala Ser Gly Leu Ile Cys Gln Pro Gln Ser Ser His Ser
 260 265 270
 Thr Thr Ser Val Cys Glu Leu Ser Ser Asn Glu Thr Arg Lys Asn Glu
 275 280 285
 Lys Glu Asp Pro Leu Asn Met Asp Glu Met Pro Phe Ile Ser Leu Ile
 290 295 300
 Pro Arg Asp Ile Leu Ser Asp Tyr Glu Glu Ser Ser Val Ile Gln Glu
 305 310 315 320
 Val Arg Lys Glu Leu Glu Ser Leu Glu Asp Gln Ala Gly Val Lys Ser
 325 330 335
 Glu His Asp Pro Ala His Asp Leu Phe Leu Gly Asp Glu Ile
 340 345 350

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 215